

1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQ 50  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 MRENMARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQ 50  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 51 QGTAALQKELKRIKIPDYSDFEKIKHLGKGHYSFYSMDIRFQLPSSQIS 100  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 51 QGTAALQKELKRIKIPDYSDFEKIKHLGKGHYSFYSMDIRFQLPSSQIS 100  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 101 MVPNVGLKESIISNANIKISGKWKAQKRFLKMSGNFDLSTIEGMSISADLKL 150  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 101 MVPNVGLKESIISNANIKISGKWKAQKRFLKMSGNFDLSTIEGMSISADLKL 150  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 151 GSNPTSGKPTITCSCSSHINSVHVIHSRSRVGWLIIQLFHRKIESALR NK 200  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 151 GSNPTSGKPTITCSCSSHINSVHVIHSRSRVGWLIIQLFHRKIESALR NK 200  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 201 MNSQVCEKVTVNSVSSKLOQYFQTLPVMTKIDSVAGINYGLVAPPATTAET 250  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 201 MNSQVCEKVTVNSVSSKLOQYFQTLPVMTKIDSVAGINYGLVAPPATTAET 250

Fig. 1

251 LDVQMRGEFYSENHNPPFAPPVMEFPAAHDMVYLGLSDYFFNTAGLV 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
251 LDVQMRGEFYSENHNPPFAPPVMEFPAAHDMVYLGLSDYFFNTAGLV 300

301 YQEAGVILKMTLRRDDMIPKESKERLTTKEFGTFLPEVAKKEPNMKIQIHVS 350  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
301 YQEAGVILKMTLRRDDMIPKESKERLTTKEFGTFLPEVAKKEPNMKIQIHVS 350

351 ASTPPPHLSVQOPTGLTFYPAVDVQAFAVLPNSSLASLFLIGM 391  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
351 ASTPPPHLSVQOPTGLTFYPAVDVQAFAVLPNSSLASLFLIGM 391

Fig. 1 (Cont.)

1 MGRQLQLWVVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSVDIF 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 MGRQLQLWVVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSVDIF 50  
  
51 KGIPFAAPTKALENPQPHPGWQGTILKAKNEFKRCLQATITQDSTYGEDDC 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 KGIPFAAPTKALENPQPHPGWQGTILKAKNEFKRCLQATITQDSTYGEDDC 100  
  
101 LYLNIIWVPQGRKQVSRLPVMWIWYGGAFLMGSGHGANFLNNYLGYDEEI 150  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 LYLNIIWVPQGRKQVSRLPVMWIWYGGAFLMGSGHGANFLNNYLGYDEEI 150  
  
151 ATRGNVIVVTENYRGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAA 200  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
151 ATRGNVIVVTENYRGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAA 200  
  
201 FGGDPNNITLFGESAGGASVSLQTLSYNKGLIRRATISQSGVALSPWVIQ 250  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
201 FGGDPNNITLFGESAGGASVSLQTLSYNKGLIRRATISQSGVALSPWVIQ 250

251 KNPLFWAKKVAEKVGCPVGDAAARMAQQCLKVTDPRALTAYKVPAGLEYP 300  
|||||  
251 KNPLFWAKKVAEKVGCPVGDAAARMAQQCLKVTDPRALTAYKVPAGLEYP 300

301 MLHYVGFVPPVIDGDFIPADPINLYANAADIDYIAGTNMDGHIEASIDMP 350  
|||||  
301 MLHYVGFVPPVIDGDFIPADPINLYANAADIDYIAGTNMDGHIEASIDMP 350

351 AINKGNKKVTEEDFYKLVSEFTITKGRAKTTFDVYTESWAQDPSQENK 400  
|||||  
351 AINKGNKKVTEEDFYKLVSEFTITKGRAKTTFDVYTESWAQDPSQENK 400

401 KKTIVVDFETDVFLVPTEIALAQHRANAKSAKTYAYLFSHPSRMPVYPKW 450  
|||||  
401 KKTIVVDFETDVFLVPTEIALAQHRANAKSAKTYAYLFSHPSRMPVYERKW 450

451 VGADHADDIQYVFGKPFATPTGYRPQDRTVSKAMIAYWWTNEAKTGDPNMG 500  
|||||  
451 VGADHADDIQYVFGKPFATPTGYRPQDRTVSKAMIAYWWTNEAKTGDPNMG 500

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Fig. 2 (Cont.)

501 DSAVPTHWEPYTTENSGYLEITKKMGSSSMKRSIRTNELRYWTLTYLALP 550  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
501 DSAVPTHWEPYTTENSGYLEITKKMGSSSMKRSIRTNELRYWTLTYLALP 550

551 TVTDQEATPVPPPTGDSEATPVPPPTGDSEATAPVPPPTGDSGAPPVPPPTGDSG 600  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
551 TVTDQEATPVPPPTGDSEATPVPPPTGDSEATAPVPPPTGDSGAPPVPPPTGDSG 600

601 APPVPPPTGDSGAPPVPPPTGDSEA 623  
||||| ||||| |||||  
601 APPVPPPTGDSGAPPVPPPTGDSGA 623

Fig. 2 (Cont.)

1 LLLLGVLSLESTLSSIPWEAPKEHKYKAEEHTVVLTVTGEPCCHFPFQY 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
4 LLLLGVLSLESTLSSIPWEAPKEHKYKAEEHTVVLTVTGEPCCHFPFQY 53  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 HRQLYHKCTHKGRPGPQPWCATTPNFDQQDQRWGYCLEPKKVVKDHCSKHSP 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
54 HRQLYHKCTHKGRPGPQPWCATTPNFDQQDQRWGYCLEPKKVVKDHCSKHSP 103  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 CQKGGTCVNMPSGPHCLCPQHILTGNHCQKEKCFFEPQLLRFFEHKNEIWYRT 150  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
104 CQKGGTCVNMPSGPHCLCPQHILTGNHCQKEKCFFEPQLLRFFEHKNEIWYRT 153  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
151 EQAAVARCQCKGPDAHCQRLASQACRTNpclHGGRCLEVEGHRLCHCPVG 200  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
154 EQAAVARCQCKGPDAHCQRLASQACRTNpclHGGRCLEVEGHRLCHCPVG 203  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
201 YTGPFCVDTKASCYDGRGLSYRGLARTTLSGAPCQQPWASEATYRNVTAE 250  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
204 YTGPFCVDTKASCYDGRGLSYRGLARTTLSGAPCQQPWASEATYRNVTAE 253  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Fig. 3

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251 QARNWGLGGHAFCRNPNDI RPWCFVLRNDRLLSWEYCDLAQCQPTQAAP 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
254 QARNWGLGGHAFCRNPNDI RPWCFVLRNDRLLSWEYCDLAQCQPTQAAP 303  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
255 QARNWGLGGHAFCRNPNDI RPWCFVLRNDRLLSWEYCDLAQCQPTQAAP 306  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
258 PTPVSPRLHVPILMPAQAPPKQOPTTRTPQSQTPGALPAKREQPPSLTR 350  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
301 PTPVSPRLHVPILMPAQAPPKQOPTTRTPQSQTPGALPAKREQPPSLTR 353  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
304 PTPVSPRLHVPILMPAQAPPKQOPTTRTPQSQTPGALPAKREQPPSLTR 353  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
351 NGPLSCGQRILRKSLSSMTRVVGGGLVALRGAHPYTAALYWGHSFCAGSLIA 400  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
354 NGPLSCGQRILRKSLSSMTRVVGGGLVALRGAHPYTAALYWGHSFCAGSLIA 403  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
401 PCWVLTAAHCLQDRPAPEDLTIVVLGQERRNHSCEPCQTLAVRSYRLHEAF 450  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
404 PCWVLTAAHCLQDRPAPEDLTIVVLGQERRNHSCEPCQTLAVRSYRLHEAF 453  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
451 SPVSYQHDLALLRIQEDADGSCALLSPYVQPVCLPSGAARPSETTLQVA 500  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
454 SPVSYQHDLALLRIQEDADGSCALLSPYVQPVCLPSGAARPSETTLQVA 503  
||||| ||||| ||||| ||||| ||||| ||||| |||||

Fig. 3 (Cont.)

501 GWGHQFEGAEYYASFLQEAQVPPFLSLERC SAPDVHGSSILPGMLCAGFILE 550  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
504 GWGHQFEGAEYYASFLQEAQVPPFLSLERC SAPDVHGSSILPGMLCAGFILE 553  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
551 GGT DACAGELLAGWRSPRSPAXSQVHSADC VFP TQGD SGGPLIVCE DQAA 600  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
554 GGT DAC.  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
601 ERR LTL QGI ISWGS GCGDRN KPGVYT DVAYYL AWIREHTVS 641  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
575 ERR LTL QGI ISWGS GCGDRN KPGVYT DVAYYL AWIREHTVS 615

Fig. 3 (Cont.)

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1 MAPFEPLASGLLILWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTP 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 MAPFEPLASGLLILWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTP 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIREFVYTPAMESVCGYFHRSH 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIREFVYTPAMESVCGYFHRSH 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 NRSEEFLLIAGKLQDGILLHITTCSFVAPWNNSLSLAQRRGFTKTYTVGCEEC 150  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 NRSEEFLLIAGKLQDGILLHITTCSFVAPWNNSLSLAQRRGFTKTYTVGCEEC 150  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
151 TVFPC 155  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
151 TVFPC 155

Fig. 4

1 MAPFEPLASGILLIWLIIAPSRACTCVPPHPQTAFCNSDLVIRAKEFVGTP 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 MAPFEPLASGILLIWLIIAPSRACTCVPPHPQTAFCNSDLVIRAKEFVGTP 50  
  
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSH 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSH 100  
  
101 NRSEEEFLIAGKLQ 113  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 NRSEEEFLIAGKLQ 113

Fig. 5

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1 MAPEEPLASGIIILWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTP 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 MAPEEPLASGIIILWLIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGTP 50  
  
51 EVNOTTLYQRYEIKMTHMYKGEQALGDAADIREVYTPAMESVCCGYFHRSH 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 EVNQTTLYQRYEIKMTHMYKGEQALGDAADIREVYTPAMESVCCGYFHRSH 100  
  
101 NRSEEFILLGKLQDGIFAHSILTCSFCWVPWENSLSLAQRQRGETKTYTVG 150  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 NRSEEFLL.AGKLQDGLL.HITTCSFV.APW.NSLSLAQRQRGETKTYTVG 146  
  
151 CEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFOQRHLACLPREPGL 200  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
147 CEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFOQRHLACLPREPGL 196  
  
201 CTWQSLRSQIA 211  
| | | | | | | |  
197 CTWQSLRSQIA 207

**Fig. 6**

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Fig.

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1 MAPFEPLASGILLIWLIAPIRACACTCVPPHPQTAFCNSDLVIRAKFVGTP 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MAPFEPLASGILLIWLIAPIRACACTCVPPHPQTAFCNSDLVIRAKFVGTP 50

51 EVNQTTLYQRYEIKMTKMYKGFAQALGDAADIRFVYTPTAMESVCGYFHR.. 98
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 EVNQTTLYQRYEIKMTKMYKGFAQALGDAADIRFVYTPTAMESVCGYFHRSH 100

99 .....AGKLQDGLLHITTCSEVAPWNSLSLAQRRGFTKTYTVGCEEC 140
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 NRSEEFILAGKLQDGGLLHITTCSEVAPWNSLSLAQRRGFTKTYTVGCEEC 150

141 TVEPCLSIPCKLQSGTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQ 190
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 TVFPCLSLIPCKLQSGTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQ 200

191 SLRSQIA 197
| | | | |
201 SLRSQIA 207

```

Fig. 8

1 MRALLARLLICVLLVSDSKGSNELHQVPSNCDCLNNGTCVSNKYFSNIHW 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 MRALLARLLICVLLVSDSKGSNELHQVPSNCDCLNNGTCVSNKYFSNIHW 50  
  
51 CNCPKKEFGQHCEIDKSRTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVL 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 CNCPKKEFGQHCEIDKSRTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVL 100  
  
101 QQTYHAHRSDALQIQLGKHNHYCREVGAQGPKAALPTVPRNLVTIPFSQRAG 150  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 QQTYHAHRSDALQIQLGKHNHYCR.....123  
  
151 HSTREVQPLVLESSLRGGREGPLGWNDIPYLSVLPGNPDNRRRPWCYVQV 200  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
124 .....NPDNRRRPWCYVQV 137  
  
201 GLKPLIVQECMVHDCADGKKPSSPPEELKFQCCQKTLRPREKITIGGEFTTI 250  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
138 GLKPLIVQECMVHDWADGKKPSSPPEELKFQCCQKTLRPREKITIGGEFTTI 187

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Fig. 9

251	ENOPWFAAIYRRHGGSVTVYCGGLISPCWVISATHCFIDYPKEDYIV	300				
		237				
188	ENOPWFAAIYRRHGGSVTVYCGGLISPCWVISATHCFIDYPKEDYIV	350				
		287				
301	YLGRSRILNSNTQGEMKFEVENLILHKDYSADTLAHNDIALLKIRSKER	400				
		337				
238	YLGRSRILNSNTQGEMKFEVENLILHKDYSADTLAHNDIALLKIRSKER	450				
		388				
351	CAQPSRTIQTICLPSMYNDPQFGTSCEITGEKENSTDYLYPEQLKMTVV	400				
		337				
288	CAQPSRTIQTICLPSMYNDPQFGTSCEITGFGENSTDYLYPEQLKMTVV	450				
		388				
401	KLISHRECQQPHYYGSEVTKMLCAADPQWKTDSCQGDGGPLVCSLQGR	400				
		388				
338	KLISHRECQQPHYYGSEVTKMLCAADPQWKTDSCQGDGGPLVCSLQGR	450				
		388				
451	MTLTGIVSWGRGCCALKDKPGVYTRVSHFLPWIRSHTEENGTL	494				
		431				
388	MTLTGIVSWGRGCCALKDKPGVYTRVSHFLPWIRSHTEENGVL	494				

Fig. 9 (cont.)

```

1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVIAHLASDFGVRVFQQVAQAS 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVIAHLASDFGVRVFQQVAQAS 50

51 KDRNVVFSPYGVASVILAMILQTTGGETQQQIQAAMGFKIDDKGMAPALRH 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 KDRNVVFSPYGVASVILAMILQTTGGETQQQIQAAMGFKIDDKGMAPALRH 100

101 LYKEILMGPWNKDEIISSTDAIFVQRLKLVQGEMPHFEFLERSTVKQVDFS 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 LYKEILMGPWNKDEIISSTDAIFVQRLKLVQGEMPHFEFLERSTVKQVDFS 150

151 EVERAREIIINDWVKIHTKGMIISNLIGKGAVDQLTRLVLNALYFNGQWKT 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 EVERAREIIINDWVKIHTKGMIISNLIGKGAVDQLTRLVLNALYFNGQWKT 200

201 PFPDSSTHRRLEHKSDGSTSVSPMMMAQTNKFYTYEFTTPDGHYYDILELP 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 PFPDSSTHRRLEHKSDGSTSVSPMMMAQTNKFYTYEFTTPDGHYYDILELP 250

251 YHGDTLMSMFIAADL...VPTEAL 270
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 YHGDTLMSMFIAAPYEKEVPLSAL 273

```

Fig. 10

1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQAS 50  
 |||||  
 1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQAS 50  
  
 51 KDRNWWFSPYGVASVILQLQTGGETQQQIQAAMGFKIDDKGMAPALRH 100  
 |||||  
 51 KDRNWWFSPYGVASVILQLQTGGETQQQIQAAMGFKIDDKGMAPALRH 100  
  
 101 LYKELMGPWNKDEIISTTDAIFVQRDLKLVQGTMMPHFERLFRSTVKQVDFS 150  
 |||||  
 101 LYKELMGPWNKDEIISTTDAIFVQRDLKLVQGTMMPHFERLFRSTVKQVDFS 150  
  
 151 EVERARFIINDWVKTHTKGMISSLGKGAVDQLTRLVNVNALYFNGQWKT 200  
 |||||  
 151 EVERARFIINDWVKTHTKGMISSLGKGAVDQLTRLVNVNALYFNGQWKT 200  
  
 201 PFPDSSTHRRLFHKS DGSTSVSPMMMAQTNKFN NYTEFTPDGHYYDILELP 250  
 |||||  
 201 PFPDSSTHRRLFHKS DGSTSVSPMMMAQTNKFN NYTEFTPDGHYYDILELP 250

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**Fig. 11**

251 YHGDTLSMFIAAAPYKEVPLSALTNIILSAQLISHWKGNMTRLPRLLVLPK 300  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
251 YHGDTLSMFIAAAPYKEVPLSALTNIILSAQLISHWKGNMTRLPRLLVLPK 300  
  
301 FSLETEVDLRKPLENLGMTDMFRQFQADFTSISDQEPLHVAQALQKVIE 350  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
301 FSLETEVDLRKPLENLGMTDMFRQFQADFTSISDQEPLHVAQALQKVIE 350  
  
351 VNESGTVASSSTAVIVSARMAPEEIMDRPFLFVV 385  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
351 VNESGTVASSSTAVIVSARMAPEEIMDRPFLFVV 385

Fig. 11 (Cont.)

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1 MTAASMGPVVRVAFVVLLALCSRPAVGQNCSPGCRCPDEPAPRCPAGVSLV 50  
1 MTAASMGPVVRVAFVVLLALCSRPAVGQNCSPGCRCPDEPAPRCPAGVSLV 50  
51 LDGGCCRVCAKQLGEIICTERDPCDPHKGLFCDFGSANRKIGVCTAKDG 100  
51 LDGGCCRVCAKQLGEIICTERDPCDPHKGLFCDFGSANRKIGVCTAKDG 100  
51 APCIFGGTVYRSGESEQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPFL 150  
101 APCIFGGTVYRSGESEQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPFL 150  
101 APCIFGGTVYRSGESEQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPFL 150  
151 P.....LEDTEGPDPMTMIRANCL 168  
151 P.....LEDTEGPDPMTMIRANCL 168  
151 PRRVKJLPGKCCCEWWVCDEPKDQTWVGPALAAAYRLEDTEGPDPMTMIRANCL 200

Fig. 12

169 VQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCESDLEENI 218  
 ||||| ||||| ||||| ||||| |||||  
 201 VQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENI 250  
 .  
 219 KKGKKCIRTPKISPKIPEELSGCTSMKTYRAKEFCGVCTDGRCCTPHRRTT 268  
 ||||| ||||| ||||| |||||  
 251 KKGKKCIRTPKISPKIPEELSGCTSMKTYRAKEFCGVCTDGRCCTPHRRTT 300  
 .  
 269 LPVEFKCPDGEVMKKNNMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 317  
 ||||| ||||| ||||| |||||  
 301 LPVEFKCPDGEVMKKNNMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

Fig. 12 (Cont..)

3 MENSIRCVWWPKLAFVLFgasllsAHLQVTGFQIKRAFTALRFLSEPSDAV 52  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 MENSIRCVWWPKLAFVLFgasllsAHLQVTGFQIKRAFTALRFLSEPSDAV 50  
 ||||| ||||| ||||| ||||| ||||| |||||  
 53 TMRGGNVLIDCSAESDRGVPVTKKKDAIHLALGMDERKQQLSNGSLLIQ 102  
 ||||| ||||| ||||| ||||| ||||| |||||  
 51 TMRGGNVLIDCSAESDRGVPVTKKKDGIIHLALGMDERKQQLSNGSLLIQ 100  
 ||||| ||||| ||||| ||||| |||||  
 103 NILHSRHHKPDEGLYQCEASLGDSGSIIISRATAKVAVAGPLRFLSQTESVT 152  
 ||||| ||||| ||||| ||||| ||||| |||||  
 101 NILHSRHHKPDEGLYQCEASLGDSGSIIISRATAKVAVAGPLRFLSQTESVT 150  
 ||||| ||||| ||||| ||||| |||||  
 153 AFMGDTVLLKCEVIGEPMPTIHWQKNQQDLTPIPGDSRVVVLPMSGALQIS 202  
 ||||| ||||| ||||| ||||| ||||| |||||  
 151 AFMGDTVLLKCEVIGEPMPTIHWQKNQQDLTPIPGDSRVVVLPMSGALQIS 200  
 ||||| ||||| ||||| |||||  
 203 RLQPQDIGTYRCSSARNPASSRTGNEAEVRILSDPGLHRQLYFLQRPSNVV 252  
 ||||| ||||| ||||| ||||| |||||  
 201 RLQPQDIGTYRCSSARNPASSRTGNEAEVRILSDPGLHRQLYFLQRPSNVV 250

Fig. 13

253 AIEGKDAVLECCVSGYPPPSFTWLGEEVIQRLRSKKYSLLGGSNLLISNV 302  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
251 AIEGKDAVLECCVSGYPPPSFTWLGEEVIQRLRSKKYSLLGGSNLLISNV 300

303 TDDDSGMYTCVVTYKNENISASAELTVLV 331  
||||| ||||| ||||| ||||| ||||| |||||  
301 TDDDSGMYTCVVTYKNENISASAELTVLV 329

Fig. 13 (Cont.)

3 MENSIRCVWVPKLAFVLFGASLLSAHLQVTGFQIKAFTALRFLSEPSDAV 52  
 1 MENSIRCVWVPKLAFVLFGASLLSAHLQVTGFQIKAFTALRFLSEPSDAV 50  
 53 TMRGGNVLLDCSAESDRGVPVTKWKKDAIHLALGMDERKQQLSNGSLLIQ 102  
 51 TMRGGNVLLDCSAESDRGVPVTKWKKDAIHLALGMDERKQQLSNGSLLIQ 100  
 103 NILHSRHHKPDEGLYQCEASLGDSGSIIISRRTAKVAVAGPLRFLSQTESVT 152  
 101 NILHSRHHKPDEGLYQCEASLGDSGSIIISRRTAKVAVAGPLRFLSQTESVT 150  
 153 AFMGDTVLLKCEVIGEPMPTIHWNQKNQQDLTPIPGDSRVVVLPSGALQIS 202  
 151 AFMGDTVLLKCEVIGEPMPTIHWNQKNQQDLTPIPGDSRVVVLPSGALQIS 200  
 203 RLQPGDIGIYRCSSARNPASSRTIGNEAEVRILSDPGLHRYQLYFLQRPSNVV 252  
 201 RLQPGDIGIYRCSSARNPASSRTIGNEAEVRILSDPGLHRYQLYFLQRPSNVV 250  
 253 AIEGKDAVLECCVSGYPPPSFTWLREEVIQLRSKKYSLLGGSNLLISNW 302  
 251 AIEGKDAVLECCVSGYPPPSFTWLREEVIQLRSKKYSLLGGSNLLISNW 300

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**Fig. 14**

303 TDDSGMYTCVVTKNENISASAELTVLVPPWFLNHPSNLYAYESMDIEF 352  
 ||||| ||||| ||||| ||||| ||||| |||||  
 301 TDDSGMYTCVVTKNENISASAELTVLVPPWFLNHPSNLYAYESMDIEF 350  
 . . . . .  
 353 ECTVSGKPVPTVNMKNGDVVVIPSDFQIVGGSNLRLILGVVKSDGIFYQC 402  
 ||||| ||||| ||||| ||||| ||||| |||||  
 351 ECTVSGKPVPTVNMKNGDVVVIPSDFQIVGGSNLRLILGVVKSDGIFYQC 400  
 . . . . .  
 403 VAENEAGNAQTSQAQLIVPKPAIPSSSVLPSAPRVDVVPVLVSSSRFVRLSWR 452  
 ||||| ||||| ||||| ||||| ||||| |||||  
 401 VAENEAGNAQTSQAQLIVPKPAIPSSSVLPSAPRVDVVPVLVSSSRFVRLSWR 450  
 . . . . .  
 453 PPAEAKGNIQQTETVFFSREGDNRERALNTTQPGSLQLTVGNLKPEAMYTF 502  
 ||||| ||||| ||||| ||||| ||||| |||||  
 451 PPAEAKGNIQQTETVFFSREGDNRERALNTTQPGSLQLTVGNLKPEAMYTF 500  
 . . . . .  
 503 RVVAYNEWGPGESSIONQPIKVATQPELQVPGPVENLQAVSTSPTSLITWEP 5.52  
 ||||| ||||| ||||| ||||| ||||| |||||  
 501 RVVAYNEWGPGESSIONQPIKVATQPELQVPGPVENLQAVSTSPTSLITWEP 550  
 . . . . .  
 553 PAYANGPVQGYRLFCTEVSTGKEQNIEDGLSYKLEGKKEFYSLRETLA 602  
 ||||| ||||| ||||| ||||| |||||  
 551 PAYANGPVQGYRLFCTEVSTGKEQNIEDGLSYKLEGKRFTEYSLRETLA 600

Fig. 14 (Cont.)

603 YNRYPGVSTDDITVVTLSDVPSAPPQNSLEVVNSRSIKVSWLPPSGT 652  
 ||||| ||||| ||||| ||||| ||||| |||||  
 601 YNRYPGVSTDDITVVTLSDVPSAPPQNSLEVVNSRSIKVSWLPPSGT 650  
 ||||| ||||| ||||| ||||| |||||  
 653 QNGFITGYKIRHRKTTRGEMETILEPNNLWYLIFTGLEKGSOYSFQVSAMT 702  
 ||||| ||||| ||||| ||||| |||||  
 651 QNGFITGYKIRHRKTTRGEMETILEPNNLWYLIFTGLEKGSOYSFQVSAMT 700  
 ||||| ||||| ||||| |||||  
 703 VNGTGPSPSNWYTAETPENDLDESQVQPDQPSLLHVRPOTNCIIMSWTPPLN 752  
 ||||| ||||| ||||| ||||| |||||  
 701 VNGTGPSPSNWYTAETPENDLDESQVQPDQPSLLHVRPOTNCIIMSWTPPLN 750  
 ||||| ||||| ||||| |||||  
 753 PNIVVRGYIIGYGGSPPYAETVRVDSKQRYYSSIERLESSSHYVLSKAFN 802  
 ||||| ||||| ||||| ||||| |||||  
 751 PNIVVRGYIIGYGGSPPYAETVRVDSKQRYYSSIERLESSSHYVLSKAFN 800  
 ||||| ||||| ||||| |||||  
 803 NAGEGVPLYESATTRSITDPTDPVDDYPLLDFFPTSVPDLSTPMMLPPVGV 852  
 ||||| ||||| ||||| ||||| |||||  
 801 NAGEGVPLYESATTRSITDPTDPVDDYPLLDFFPTSVPDLSTPMMLPPVGV 850  
 ||||| ||||| ||||| |||||  
 853 QAVALTHDAVRVSWADNSVPKNQKTSEVRLYTVRWRTSFSASAKYKSEDT 902  
 ||||| ||||| ||||| |||||  
 851 QAVALTHDAVRVSWADNSVPKNQKTSEVRLYTVRWRTSFSASAKYKSEDT 900

Fig. 14 (Cont.)

903 TLSYATGLKPNTMYYEF SVMKNRSSSTWSMTAHTTYEAAPTSAPKD 952  
 |||||  
 901 TLSYATGLKPNTMYYEF SVMKNRSSSTWSMTAHTTYEAAPTSAPKD 950  
 |||||

953 FTVITREGKPRAVIVSWQPPLEANGKITAYILFYTLDFKNIPIDDWIMETI 1002  
 |||||  
 951 FTVITREGKPRAVIVSWQPPLEANGKITAYILFYTLDFKNIPIDDWIMETI 1000  
 |||||

1003 SGDRLTHQIMDLNLDTMYYFRIQARNSKVGVLGPLSDPILFRTLKVEHPDKM 1052  
 |||||  
 1001 SGDRLTHQIMDLNLDTMYYFRIQARNSKVGVLGPLSDPILFRTLKVEHPDKM 1050  
 |||||

1053 ANDQGRHGDGGYW PVDTNLIDRSTLNEPPIGQMHPHGSVTPQKNSNLLV 1102  
 |||||  
 1051 ANDQGRHGDGGYW PVDTNLIDRSTLNEPPIGQMHPHGSVTPQKNSNLLV 1100  
 |||||

1103 IIVVTVGVI TVVVIVAVICTRSSAQQRKKRATHSAGKRKGSQKDLRP 1152  
 |||||  
 1101 IIVVTVGVI TVVVIVAVICTRSSAQQRKKRATHSAGKRKGSQKDLRP 1150  
 |||||

1153 PDLWIHHEEMEMKNI EKPSGTDPAGRDSPIQSCQDLTPVSHSQSETQLGS 1202  
 |||||  
 1151 PDLWIHHEEMEMKNI EKPSGTDPAGRDSPIQSCQDLTPVSHSQSETQLGS 1200  
 |||||

Fig. 14 (Cont.)

1203 KSTSHSGQDTEEAQSSMSTLERSLAARRAPRAKLMIPMDAQSNNPAAVVA 1252  
 ||||| ||||| ||||| ||||| |||||  
 1201 KSTSHSGQDTEEAQSSMSTLERSLAARRAPRAKLMIPMDAQSNNPAAVVA 1250  
 ||||| ||||| ||||| |||||  
 1253 IPVPTLESAQYPGTILPSSPTCGYYPHPQFTTLRPVPPFPTLSVDRGFGAGRSQS 1302  
 ||||| ||||| ||||| |||||  
 1251 IPVPTLESAQYPGTILPSSPTCGYYPHPQFTTLRPVPPFPTLSVDRGFGAGRSQS 1300  
 ||||| ||||| |||||  
 1303 VSEGPTTQQPPMLPPSQPEHSSSEEAPSRTIPTACVRPTHPLRSEANPLL 1352  
 ||||| ||||| ||||| |||||  
 1301 VSEGPTTQQPPMLPPSQPEHSSSEEAPSRTIPTACVRPTHPLRSEANPLL 1350  
 ||||| ||||| |||||  
 1353 PPPMSAIEPKVVPYTPILLSQPGPTLPKTHVKTAISLGLACKARSPLLPVSVP 1402  
 ||||| ||||| ||||| |||||  
 1351 PPPMSAIEPKVVPYTPILLSQPGPTLPKTHVKTAISLGLACKARSPLLPVSVP 1400  
 ||||| |||||  
 1403 TAPEVSEESHKPTEDSANV 1421  
 ||||| ||||| |||||  
 1401 TAPEVSEESHKPTEDSANV 1419

Fig. 14 (Cont.)

1 MPGKRGGLGWWARLPLCLLSSLYGPWMPSSLGKPKGHPMNSIRIDGDT 50  
 |||||  
 1 MPGKRGGLGWWARLPLCLLSSLYGPWMPSSLGKPKGHPMNSIRIDGDT 50  
 |||||  
 51 LGGLEFPVHGRGSEKGKPCGELKKEKGTHRLEAMLFALDRINNDPDLLPNIT 100  
 |||||  
 51 LGGLEFPVHGRGSEKGKPCGELKKEKGTHRLEAMLFALDRINNDPDLLPNIT 100  
 |||||  
 101 LGARILDTCRDTHALEQSLTENVQALIEKDGTENVRCGGPPIITKPERV 150  
 |||||  
 101 LGARILDTCRDTHALEQSLTENVQALIEKDGTENVRCGGPPIITKPERV 150  
 |||||  
 151 VGVIGASGSSVSVIMVANILRLFKIPQISYASTAPDLSDNSRYDEFSRVVP 200  
 |||||  
 151 VGVIGASGSSVSVIMVANILRLFKIPQISYASTAPDLSDNSRYDEFSRVVP 200  
 |||||  
 201 SDTYQAQAMVDIVRALKNNYVSTVASEGSYGESGVEAFIQKSREDDGGVCI 250  
 |||||  
 201 SDTYQAQAMVDIVRALKNNYVSTVASEGSYGESGVEAFIQKSREDDGGVCI 250  
 |||||  
 251 AQSVVKIPREPCKAGEFDKIIIRRLLETSNARAVITIFANEDDIRVLEARRA 300  
 |||||  
 251 AQSVVKIPREPCKAGEFDKIIIRRLLETSNARAVITIFANEDDIRVLEARRA 300

Fig. 15

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Fig. 15 (Cont.)

554 ATLFVWITFVRYNDTPIVKASGRELSYVLLAGIFLCYATTFLMIAEPDILG 603  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 601 ATLFVWITFVRYNDTPIVKASGRELSYVLLAGIFLCYATTFLMIAEPDILG 650  
  
 604 TCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRSSVSAFRFISPA SQL 653  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 651 TCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGKRSSVSAFRFISPA SQL 700  
  
 654 AITESLISLQLLGICWWEVVDPSSHVVDFQDQRTLDPREFARGVLKCDISD 703  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 701 AITESLISLQLLGICWWEVVDESHSVVVDFQDQRTLDPREFARGVLKCDISD 750  
  
 704 LSLICLIGYSMLIMVTCTVYAIKTRGVPETENEAKPIGFTMYTCIVWIA 753  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 751 LSLICLIGYSMLIMVTCTVYAIKTRGVPETENEAKPIGFTMYTCIVWIA 800

Fig. 15 (Cont.)

754 FIPIFEGTSQSADKLYIQTTTIVSVSISASVSLGMLYMPKVVYILFHPE 803  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
801 FIPIFEGTSQSADKLYIQTTTIVSVSISASVSLGMLYMPKVVYILFHPE 850

804 QNVPKRKRSILKAVVTAATMSNKFTQKGNGERPNGEAKSELCEAPALAT 853  
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
851 QNVPKRKRSILKAVVTAATMSNKFTQKGNGERPNGEAKSELCEAPALAT 900

854 KQTYYVTYTNHAI 865  
||||| ||||| |||||  
901 KQTYYVTYTNHAI 912

**Fig. 15 (Cont.)**

```

1 METKGYHSLPEGLDMERRWGQVSQAVERSSLGPPTERTDENNYMEIVNVSC 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
1 METKGYHSLPEGLDMERRWGQVSQAVERSSLGPPTERTDENNYMEIVNVSC 50

51 VSGAIPNNSTQGSSKEKQELLPCLQQDNNRPGILTSDIKTELESKELSAT 100
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
51 VSGAIPNNSTQGSSKEKQELLPCLQQDNNRPGILTSDIKTELESKELSAT 100

101 VAESMGLYMDSVRDADYSYEQQNQQGMSPAKIYQNVEQLVKFYKGNGHR 150
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
101 VAESMGLYMDSVRDADYSYEQQNQQGMSPAKIYQNVEQLVKFYKGNGHR 150

151 PSTLSCVNTPLRSEMSDGSVNGGVMRATVKSPIMCHEKSPSVCSPLN 200
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
151 PSTLSCVNTPLRSEMSDGSVNGGVMRATVKSPIMCHEKSPSVCSPLN 200

201 TSSVCSPAGINSVSSTTASFGSEPVHSPITQGTPLTCS PNAENRGSRSHS 250
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
201 TSSVCSPAGINSVSSTTASFGSEPVHSPITQGTPLTCS PNAENRGSRSHS 250

251 PAHASNVGSPLISSPLISSMKSSISPPSHCSVKSPVSSPNNVTLRSSVSSP 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
251 PAHASNVGSPLISSPLISSMKSSISPPSHCSVKSPVSSPNNVTLRSSVSSP 300

```

Fig. 16

301 ANINNSRCVSSPSNTNNRSTLSSPAASTVGSTICSPVNNAFSYTAGTSA 350  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 301 ANINNSRCVSSPSNTNNRSTLSSPAASTVGSTICSPVNNAFSYTAGTSA 350  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 351 GSSTLRDVVPS PDTQEKGQAQEVFPKTEEVEESAISNGVTGQLNIVQYIKP 400  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 351 GSSTLRDVVPS PDTQEKGQAQEVFPKTEEVEESAISNGVTGQLNIVQYIKP 400  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 401 EPDGAFSSSCLGGNSKINSDSSFSVPIKQUESTKHSCSGTSFKGNPTVNPF 450  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 401 EPDGAFSSSCLGGNSKINSDSSFSVPIKQUESTKHSCSGTSFKGNPTVNPF 450  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 451 PFMDSYFSEMDDKDYSLSGILGPPVPGEFDGNCCEGSGFPVGKQEPDDG 500  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 451 PFMDSYFSEMDDKDYSLSGILGPPVPGEFDGNCCEGSGFPVGKQEPDDG 500  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 501 SYYPEASIPSSAIVGVNNGGQSFHYRIGAQGTISLSRSARDQSFQHLSSF 550  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 501 SYYPEASIPSSAIVGVNNGGQSFHYRIGAQGTISLSRSARDQSFQHLSSF 550  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 551 PPVNTLVEWKSHGDLSSRRSDGYPVLEYIPEENVSSSTLRSVSTGSSRPS 600  
 ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 551 PPVNTLVEWKSHGDLSSRRSDGYPVLEYIPEENVSSSTLRSVSTGSSRPS 600

Fig. 16 (Cont.)

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601 KICLVC GDEA SGCH YGVV TGSCKV FFKRAVE QHNYL CAGR NDCT IDKI 650  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
601 KICLVC GDEA SGCH YGVV TGSCKV FFKRAVE QHNYL CAGR NDCT IDKI 650  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
651 RRKN CPACR LQKCL QAGM NLGARK SKKL GKLKG IHEEQ PQQQQ PPPPPP 700  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
651 RRKN CPACR LQKCL QAGM NLGARK SKKL GKLKG IHEEQ PQQQQ PPPPPP 700  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
701 PQSPEEGTTYI A PAK E P S V N T A L V P Q L S T I S R A L T P S P V M V L E N I E P E I V 750  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
701 PQSPEEGTTYI A PAK E P S V N T A L V P Q L S T I S R A L T P S P V M V L E N I E P E I V 750  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
751 YAGY DSSSKPDTAENL I S T I N R L A G K Q M I Q V V K W A K V L P G F K N I P L E D Q I T 800  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
751 YAGY DSSSKPDTAENL I S T I N R L A G K Q M I Q V V K W A K V L P G F K N I P L E D Q I T 800  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
801 LIQYSWMCLSSFA LSWRSYKHTNSQFLYFAPDLVFNE 837  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
801 LIQYSWMCLSSFA LSWRSYKHTNSQFLYFAPDLVFNE 837

**Fig. 16 (Cont.)**

1 METKGYHSLPEGLDMERRWGQVSAVERSSLGPTERTDENNYMEIVNVSC 50  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 METKGYHSLPEGLDMERRWGQVSAVERSSLGPTERTDENNYMEIVNVSC 50  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 51 VSGAIPNNSTQGSSKEKQELLPCLQQDNNRPGIILTSDIKTELESKELSAT 100  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 51 VSGAIPNNSTQGSSKEKQELLPCLQQDNNRPGIILTSDIKTELESKELSAT 100  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 101 VAESMGLYMDSVRDADYSYEQQNQQGSMSPAKIYQNVEQLVKFYKGNGHR 150  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 101 VAESMGLYMDSVRDADYSYEQQNQQGSMSPAKIYQNVEQLVKFYKGNGHR 150  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 151 PSTLSCVNTPLRSEMSDSGSSVNGGVMRAlVKSPIMCHEKSPSVCSPLNM 200  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 151 PSTLSCVNTPLRSEMSDSGSSVNGGVMRAlVKSPIMCHEKSPSVCSPLNM 200  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 201 TSSVCPAGINSVSSTSASFGSFPVHSPITQGTPLTCSPNAENRGSRSHS 250  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 201 TSSVCPAGINSVSSTSASFGSFPVHSPITQGTPLTCSPNAENRGSRSHS 250  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 251 PAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLLRSSVSSP 300  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 251 PAHASNVGSPLSSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLLRSSVSSP 300

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Fig. 17

301	ANINNSRCVSSSPSNTNNRSTLSSPAASTVGSTICSPVNNAFSYTA 350
301	ANINNSRCVSSSPSNTNNRSTLSSPAASTVGSTICSPVNNAFSYTA 350
351	GSSTLRDVVPSPDQTQEKGAEVPEPKTEEVESAISNGV'TGQLNIVQYIKP 400
351	GSSTLRDVVPSPDQTQEKGAEVPEPKTEEVESAISNGV'TGQLNIVQYIKP 400
401	EPDGAFSSSCLGGNSKINSDSSFSVPIKQUESTKHSCSGTSEFKGNPTVNPF 450
401	EPDGAFSSSCLGGNSKINSDSSFSVPIKQUESTKHSCSGTSEFKGNPTVNPF 450
451	PFMDGSYFSEWDDKDYYLSGILGPPVPGFDGNCCEGSGFPVGKQEPDDG 500
451	PFMDGSYFSEWDDKDYYLSGILGPPVPGFDGNCCEGSGFPVGKQEPDDG 500
501	SYYPEASIPSSATVGVNNSGGQSEHYRIGAQGTISLRSARDQSFQHLS 550
501	SYYPEASIPSSATVGVNNSGGQSEHYRIGAQGTISLRSARDQSFQHLS 550
551	PPVNNTLVESWKSHGDISSRRSDGYPVIEYIPENVS 600
551	PPVNNTLVESWKSHGDISSRRSDGYPVIEYIPENVS 600

Fig. 17 (Cont..)

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601	KICLVCGDEASGCHYGVVTGSCKVFKRAVEQHNYLCAGRNDCTIDKI	650
601	KICLVCGDEASGCHYGVVTGSCKVFKRAVEQHNYLCAGRNDCTIDKI	650
651	RRKNCACRLQKCLQAGMNLGARKSKLGLKGTHEEQPQQQQPPPPPPP	700
651	RRKNCACRLQKCLQAGMNLGARKSKLGLKGTHEEQPQQQQPPPPPPP	700
701	PQSPEEGTTIYAAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIV	750
701	PQSPEEGTTIYAAPAKEPSVNTALVPQLSTISRALTPSPVMVLENIEPEIV	750
751	YAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKAVALPGEKNLPLEDQIT	800
751	YAGYDSSKPDTAENLLSTLNRLAGKQMIQVVKAVALPGEKNLPLEDQIT	800
801	LIQYSWMCLSSFEALSWRSYKHTNSQFLYFAPDLVNE	837
801	LIQYSWMCLSSFEALSWRSYKHTNSQFLYFAPDLVNE	837

Fig. 17 (Cont.)

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1	MGRQLQLVVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSVDIF	50
1	MGRQLQLVVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSVDIF	50
51	KGIPFAAPTKALENPQOPHPGWWQGTLKAKNFKKRCLQATITQDSTYGEDDC	100
51	KGIPFAAPTKALENPQOPHPGWWQGTLKAKNFKKRCLQATITQDSTYGEDDC	100
101	LYLNIWVPQGRKQVSRDLPVMIWIYGGAFLMGSGHGANFLNNYLYDGEI	150
101	LYLNIWVPQGRKQVSRDLPVMIWIYGGAFLMGSGHGANFLNNYLYDGEI	150
151	ATRGNVIVVTNFNYRVGPLGELSTGDANLPGNYGLRDQHMAIAAWVKRNIAA	200
151	ATRGNVIVVTNFNYRVGPLGELSTGDANLPGNYGLRDQHMAIAAWVKRNIAA	200
201	FGGDPNNITLFGESAGGASVSLQTISPYNKGLIRRAlSQSGVALSPWVIQ	250
201	FGGDPNNITLFGESAGGASVSLQTISPYNKGLIRRAlSQSGVALSPWVIQ	250

**Fig. 18**

251 KNPLFWARKVVAEKVGCPVGDAARMAQCLKVTDPRALTLAYKVPLAGLEYP 300  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 251 KNPLFWARKVVAEKVGCPVGDAARMAQCLKVTDPRALTLAYKVPLAGLEYP 300  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 301 MLHYVGFPVTDGDFIPADPINLYANAADIIDYIAGTNMDGHIFASIDMP 350  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 301 MLHYVGFPVTDGDFIPADPINLYANAADIIDYIAGTNMDGHIFASIDMP 350  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 351 AINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTEDVYTESWAQDPSQENK 400  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 351 AINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTEDVYTESWAQDPSQENK 400  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 401 KKTVVDFETDVLFVPTEIALAQHRANAKSAKTYAYLFSHPSRMPVYPKW 450  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 401 KKTVVDFETDVLFVPTEIALAQHRANAKSAKTYAYLFSHPSRMPVYPKW 450  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 451 VGADHADDIQYVFGKPFEATPTGYRPQDRTVSKAMIAYWTNFAKTAGDPNMG 500  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 451 VGADHADDIQYVFGKPFEATPTGYRPQDRTVSKAMIAYWTNFAKTAGDPNMG 500  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Fig. 18 (Cont. <sup>1</sup>)

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Fig. 18 (cont.)

1 MRALLARLLCVLVVSDSKGSNELHQVPSNCDCLNNGTCVSNKYFSNIHW 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 MRALLARLLCVLVVSDSKGSNELHQVPSNCDCLNNGTCVSNKYFSNIHW 50  
  
51 CNCPPKKFEGGQHCEIDKSKTCYEGNGHFYRGKASTDDTMGRPCLPWN SATVL 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 CNCPPKKFEGGQHCEIDKSKTCYEGNGHFYRGKASTDDTMGRPCLPWN SATVL 100  
  
101 QQTYHAHRSDALQLGLGKHNYCR 123  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 QQTYHAHRSDALQLGLGKHNYCR 123

**Fig. 19**

1 MKTYRAKFCGVCTDGRCCCTPHRTTLPVEFKCPDGEVMKKNNMMFIKTCAC 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
276 MKTYRAKFCGVCTDGRCCCTPHRTTLPVEFKCPDGEVMKKNNMMFIKTCAC 325

51 HYNCPGNDNIDFESLYYRKMYGDMA 74  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
326 HYNCPGNDNIDFESLYYRKMYGDMA 349

Fig. 20

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Fig. 21

1 MENSLLRCVWWPKLAFVILFGASILLSAHLQVTGEQIKAFTALRELSEPSDAV 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 MENSLLRCVWWPKLAFVILFGASILLSAHLQVTGEQIKAFTALRELSEPSDAV 50

51 TMRGGGNVLLDCSAESDRGVPVIIKWKKDCIHLALGMDERKQQLSNGSILLIQ 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
51 TMRGGGNVLLDCSAESDRGVPVIIKWKKDCIHLALGMDERKQQLSNGSILLIQ 100

101 NILHSRHHKPDEGLYQCEASILGDSGSIIISRTAKVAVAGP 139  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
101 NILHSRHHKPDEGLYQCEASILGDSGSIIISRTAKVAVAGP 139

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Fig. 22

Fig. 23

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Fig. 24

1	MAPFEPLASGILLIWLIIAPSRACTCVPPHPQTAFCNSDLVIRAKFVGT P	50
51	EVNQTTLYQRYEIKMTKMYKGEQALGDAADIRFVYT PAMESVCGYFHR	98
51	EVNQTTLYQRYEIKMTKMYKGEQALGDAADIRFVYT PAMESVCGYFHR	98

Fig. 25

1 MTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFILAGKLQD 50  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
65 MTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFILAGKLQD 114  
  
51 GLLHITTCSFWAPWNNSLIAQRRGFTKTYTVGCEEECTVFPCLSIPCKLQS 100  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
115 GLLHITTCSFWAPWNNSLIAQRRGFTKTYTVGCEEECTVFPCLSIPCKLQS 164  
  
101 GTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQSLRSQIA 143  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
165 GTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQSLRSQIA 207

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Fig. 26